



1600

RAW SEQUENCE LISTING

DATE: 09/09/2003

PATENT APPLICATION: US/09/347,064H

TIME: 16:44:48

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\09092003\I347064H.raw

W--> Substitute SL (09.02.03) *delete*

5 <110> APPLICANT: Eck, Jurgen
 6 Schmidt, Arno
 7 Zinke, Holger
 9 <120> TITLE OF INVENTION: Recombinant Fusion Proteins Based on Ribosome-Inactivating
 Proteins of

10 the Mistletoe Viscum album
 12 <130> FILE REFERENCE: 09282-5
 14 <140> CURRENT APPLICATION NUMBER: 09/347,064H
 15 <141> CURRENT FILING DATE: 1999-07-02
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP98/00009
 18 <151> PRIOR FILING DATE: 1998-01-02
 20 <150> PRIOR APPLICATION NUMBER: EP 97 10 0012.0
 21 <151> PRIOR FILING DATE: 1997-01-02
 23 <160> NUMBER OF SEQ ID NOS: 49
 25 <170> SOFTWARE: PatentIn version 3.2
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 762
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Viscum album
 32 <400> SEQUENCE: 1

**Does Not Comply
 Corrected Diskette Needed**

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33 catatgtacg aacgtatccg tctgcgtggt acccaccaga ccaccggtga agaatatattc 60
35 cggttcatca cgcttctccg agattatgtc tcaagcggaa gcttttccaa tgagataacca 120
37 ctcttgctgc agtctacgat ccccgctctcc gatgcgcgaaa gatttgtctt ggtggagctc 180
39 accaaccagg ggggagactc gatcacggcc gccatcgacg ttaccaatct gtacgtcgtg 240
41 gcttaccagc caggcgacca atcctacttt ttgcgcgacg caccacgcgg cgcggaacg 300
43 catctcttca ccggcaccac ccgacccctc ctcccattca acggaagcta ccctgatctg 360
45 gagcgatagc ccggacatag ggaccagatc cctctcggtg tagaccaact cattcaatcc 420
47 gtcacggcgc ttcgttttcc gggcggcagc acgcgtaccc aagctcgttc gattttaatc 480
49 ctcattcaga tgatctccga ggccgccaga ttcaatccca tcttatggag ggctcgccaa 540
51 tacattaaca gtggggcgctc atttctgcca gacgtgtaca tgctggagct ggagacgagt 600
53 tggggccaac aatccacgca agtccagcat tcaaccgatg gcgtttttta taaccacaatt 660
55 cggttggcta tcccccccg gtaacttcgtg acgttgacca atgttcgcga cgtgatcgcc 720
57 agcttgccga tcatgttggt tgtatgcgga gagcgcccga gt 762

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 61 <211> LENGTH: 252
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Viscum album
 65 <400> SEQUENCE: 2
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 67 1 5 10 15
 69 Glu Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly
 70 20 25 30
 72 Ser Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val

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73          35          40          45
75 Ser Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly
76          50          55          60
78 Asp Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala
79 65          70          75          80
81 Tyr Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly
82          85          90          95
84 Ala Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe
85          100          105          110
87 Asn Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln
88          115          120          125
90 Ile Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg
91          130          135          140
93 Phe Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu
94 145          150          155          160
96 Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg
97          165          170          175
99 Ala Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr
100          180          185          190
102 Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
103          195          200          205
105 His Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro
106          210          215          220
108 Pro Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser
109 225          230          235          240
111 Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro
112          245          250
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116 <211> LENGTH: 828
117 <212> TYPE: DNA
118 <213> ORGANISM: Viscum album
120 <400> SEQUENCE: 3
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123 ggtcgaaatg gcatgtgctg ggacgtccga gatgacgatt tccgcgatgg aaatcagata 120
125 cagtgtgtgg cctccaagtc caacaatgat ccgaatcagt tgtggacgat caaaagggat 180
127 ggaaccattc gatccaatgg cagctgcttg accacgtatg gctatactgc tggcgtctat 240
129 gtgatgatct tcgactgtaa tactgctgtg cgggaggcca ctctttggca gatatggggc 300
131 aatgggacca tcatcaatcc aagatccaat ctggttttgg cagcatcatc tggaatcaaa 360
133 ggcactacgc ttacggtgca aacactggat tacacgttgg gacagggctg gcttgccggt 420
135 aatgataccg ccccacgcga ggtgaccata tatgggttca gggacctttg catggaatca 480
137 aatggaggga gtgtgtgggt ggagacgtgc gtgagtagcc aaaagaacca aagatgggct 540
139 ttgtacgggg atggttctat acgccccaaa caaaaccaag accaatgcct cacctgtggg 600
141 agagactccg tttcaacagt aatcaatata gttagctgca gcgctggatc gtctgggcag 660
143 cgatgggtgt ttaccaatga aggggccatt ttgaatttaa agaatgggtt ggccatggat 720
145 gtggcgcaag caaatccaaa gctccgccga ataatcatct atcctgccac aggaaaacca 780
147 aatcaaatgt ggcttcccgt gccagggtgga tatcactagt aaggatcc 828
150 <210> SEQ ID NO: 4
151 <211> LENGTH: 267
152 <212> TYPE: PRT

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155 <400> SEQUENCE: 4
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159 Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly
160           20           25           30
162 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
163   35           40           45
165 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
166   50           55           60
168 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
169  65           70           75           80
171 Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
172           85           90           95
174 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
175           100          105          110
177 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
178           115          120          125
180 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
181           130          135          140
183 Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
184 145           150          155          160
186 Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu
187           165          170          175
189 Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
190           180          185          190
192 Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys
193           195          200          205
195 Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala
196           210          215          220
198 Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn
199 225           230          235          240
201 Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn
202           245          250          255
204 Gln Met Trp Leu Pro Val Pro Gly Gly Tyr His
205           260          265
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 72
210 <212> TYPE: DNA
211 <213> ORGANISM: Viscum album
213 <400> SEQUENCE: 5
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216 gatgttacat gt                                                    72
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 17
221 <212> TYPE: PRT
222 <213> ORGANISM: Viscum album
224 <400> SEQUENCE: 6
226 Ser Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Arg Val Ile

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227 1          5          10          15
230 Ala
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235 <211> LENGTH: 756
236 <212> TYPE: DNA
237 <213> ORGANISM: Viscum album
239 <400> SEQUENCE: 7
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242 atcacgcttc tccgagatta tgtctcaagc ggaagctttt ccaatgagat accactcttg      120
244 cgtcagtcga cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac      180
246 caggggggag actcgatcac ggccgccatc gacgttacca atctgtacgt cgtggcttac      240
248 caagcaggcg accaatccta ctttttgcg gacgcaccac gcggcgcgga aacgcattctc      300
250 ttcaccggca ccaccgcatc ctctctccca ttcaacggaa gctaccctga tctggagcga      360
252 tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg      420
254 gcgcttcggt ttccggggcg cagcacgcgt acccaagctc gttcgatttt aatcctcatt      480
256 cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggctcg ccaatacatt      540
258 aacagtgggg cgtcatttct gccagacgtg tacatgctgg agctggagac gagttggggc      600
260 caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcgggtg      660
262 gctatacccc ccggtaaactt cgtgacgttg accaatgttc gcgacgtgat cgccagcttg      720
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268 <211> LENGTH: 252
269 <212> TYPE: PRT
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272 <400> SEQUENCE: 8
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276 Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly Ser
277          20          25          30
279 Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
280          35          40          45
282 Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp
283          50          55          60
285 Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr
286          65          70          75          80
288 Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala
289          85          90          95
291 Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
292          100          105          110
294 Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
295          115          120          125
297 Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
298          130          135          140
300 Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile
301          145          150          155          160
303 Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
304          165          170          175
306 Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
307          180          185          190

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309 Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His
310      195      200      205
312 Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
313      210      215      220
315 Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
316 225      230      235      240
318 Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser
319      245      250
323 <210> SEQ ID NO: 9
324 <211> LENGTH: 789
325 <212> TYPE: DNA
326 <213> ORGANISM: Viscum album
328 <400> SEQUENCE: 9
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331 tgcgtggacg tccgagatga cgatttccgc gatggaaatc agatacagtt gtggccctcc      120
333 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc      180
335 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac      240
337 tgtaatactg ctgtgcggga ggccactctt tggcagatat ggggcaatgg gaccatcatc      300
339 aatccaagat ccaatctggt tttggcagca tcatctggaa tcaaaggcac tacgcttacg      360
341 gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgcccc      420
343 cgcgaggtga ccatatatgg gttcaggac ctttgcattg aatcaaattg agggagtgtg      480
345 tgggtggaga cgtgcgtgag tagccaaaag aaccaaatga gggctttgta cggggatggt      540
347 tctatacgcc ccaaacaaaa ccaagaccaa tgcctcacct gtgggagaga ctccgtttca      600
349 acagtaatca atatagttag ctgcagcgct ggatcgctcg ggcagcgatg ggtgtttacc      660
351 aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaaat      720
353 ccaaagctcc gccgaataat catctatcct gccacaggaa aaccaaataca aatgtggcct      780
355 cccgtgcca      789
358 <210> SEQ ID NO: 10
359 <211> LENGTH: 263
360 <212> TYPE: PRT
361 <213> ORGANISM: Viscum album
363 <400> SEQUENCE: 10
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367 Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Asp Phe Arg Asp Gly
368      20      25      30
370 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
371      35      40      45
373 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
374      50      55      60
376 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
377 65      70      75      80
379 Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
380      85      90      95
382 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
383      100      105      110
385 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
386      115      120      125
388 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr

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VERIFICATION SUMMARY

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